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Inheritance of Some Growth Parameters in Bread Wheat

Naeem Mahmood and Muhammad Aslam Chowdhry
Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad-38040, Pakistan

Abstract

A full diallel cross involving six bread wheat genotypes was evaluated for the inheritance of some growth parameters. Mean values displayed significant reduction of 17.50, 20.60, 17.67, 15.54, 15.25 and 28.04 per cent for days to heading, plant height, fertile tillers, days to maturity, grain filling period (GFP) and grain yield per plant under late planting, respectively, as compared to normal planting. Genetic analysis revealed that additive gene action for days to heading and maturity and grain filling period under normal planting changed to dominant under late planting, while overdominant gene action for plant height changed to additive and additive gene action for fertile tillers per plant and grain yield per plant remained unchanged. Dominant genes were responsible for early heading, fertile tillers per plant and GFP under both plantings while dominant gene control for plant height and days to maturity under normal planting changed to recessive under late planting. Similarly, gene control for grain yield per plant changed from recessive to dominant under late planting.

Introduction

Crop season of wheat ranges from 145 to 150 days for normally planted crop in Pakistan. The important/critical growth stages include tillering, booting, heading, anthesis/pollination, grain formation and maturity. Heading (emergence of spike) indicates the completion of vegetative phase and onset of reproductive phase of wheat plant development. It starts after about 100 days of sowing and it takes further 5-6 days to start anthesis & pollination. The period from anthesis/palliation to maturity is the grain formation process which is termed as grain filling period (GFP).

Duration of GFP is the most significant factor affecting the quality of wheat grain. A longer GFP enables the plant to store assimilates/metabolites (carbohydrates, proteins, etc.) in the grains for longer period that results in a healthier grain with more grain weight. Time of planting wheat crop in this connection is of extreme importance. Grain yield of wheat is determined in part by grain weight which is a function of the rate and duration of grain filling (Mou and Kronstad, 1994). Thus, variation in the duration of spike emergence and maturity will obviously alter GFP which eventually affect the grain yield. GFP may be useful physiological selection trait for influencing grain yield of cereals. The significant effect of date of sowing on GFP has been reported (Sharma, 1994).

Understanding the genetic behaviour of these parameters would, thus, help to develop breeding strategies for improving wheat genotypes. Begum and Saifuzzaman (1987) observed significant influence of sowing dates on GFP and grain weight. When wheat was sown in November, GFP ranged from 45-50 days with a grain weight of 53-55 mg/grain. Late planting reduced the GFP to 20-35 days.

Khurana *et al.* (1983) reported additive genetic control for days to heading and tillers per plant. However, Singh *et al.* (1987) observed that both additive and non-additive genetic effects were important in the inheritance of ear emergence.

Partial dominant gene effects for plant height and overdominance for tiller number was recorded by Lonc (1989). Tandon *et al.* (1989) reported additive gene control for days to heading, plant height and non-additive for tiller number. Khan and Bajwa (1990) observed additive gene control for days to heading and plant height.

Genetic information regarding GFP and days to maturity has been much scarce. Present study was, therefore, undertaken to find out the patterns of inheritance for growth parameters for normally as well as late planted wheat crop which will yield useful information for future breeding strategies.

Materials and Methods

The experiment comprised six wheat genotypes viz., Pak.81, LU26S, Faisalabad 85 (Fsd.85), Pasban 90 (Psbn.90), 4943 and 4072 crossed in a 6 × 6 full diallel fashion during the crop season 1995-96.

Experimental material (all 30 F_1s along with their parents) was planted on 15th November (normal planting) while the same material was also sown on 15th December (late planting) in a triplicated randomized complete block design during the next crop season (1996-97). Plant to plant and row to row spacings were 15 and 25 cm, respectively. Seeds were sown in holes (made with the help of dibble) at the rate of 2 seeds per site which were later thinned to single healthy seedling per site after germination. Each treatment was a single line of 5 meter length comprising of approximately 30 plants. All the other cultural operations including hoeing, weeding, irrigation, fertilizers, etc. were carried out identically to reduce experimental error.

Data regarding days to heading, plant height, number of fertile tillers per plant, days to maturity, grain filling period (GFP) and grain yield per plant were collected separately from each experiment. Days to heading were counted from the date of sowing to the date of 50 per cent heading. Days to maturity were counted from date of sowing to the date of physiological maturity. Period from the date of 50

per cent anthesis to the date of maturity was counted as grain filling period in days. Data collected were subjected to analysis of variance according to Steel and Torrie (1984), separately. Formal diallel analysis as suggested by Mather and Jinks (1982) was conducted to investigate gene action and degree of dominance. Graphical analysis and computation of genetic components of variation were also carried out according to Hayman (1957).

To fulfill the assumptions of Hayman (1957) for the adequacy of additive-dominance model two tests were employed. The first test was an analysis of regression coefficient. Variances (of each array) and covariances (array with its parental values) were estimated from the mean diallel table. Then the regression of covariance on the variances was computed. According to Mather and Jinks (1982) the regression coefficient is expected to be significantly different from zero but not from unity. Failure of this test indicate presence of non-allelic interaction (epistasis) or genes are not independent in their action, or show non-random association among parents.

The second test was the analysis of variance of the Wr + Vr and Wr-Vr. If dominance (or certain types of non-allelic interaction) is present Wr + Vr must change from array to array. Similarly, if there exists epistasis, Wr-Vr will vary between arrays.

Results and Discussion

Analysis of variance revealed highly significant differences among genotypes for all the characters studied under both normal and late plantings. On overall mean basis a considerable reduction in all parameters was recorded under late planting as compared to normal planting (Table 1). Days to heading, plant height, number of fertile tillers per plant, days to maturity and grain filling period showed a reduction of 17.50, 20.60, 17.67, 15.54 and 15.25 percent, respectively. Finally grain yield per plant showed a reduction of 28.04 percent under late planting.

Days to heading: Analysis of variance (Table-2) depicted that under both normal and late plantings, item a, which measures additive gene effects, was highly significant and accounted for a high proportion of the total variation. The overall dominance component b was smaller but also highly

significant indicating the important role of dominance. The item b_1 (directional dominance deviations of the genes) was significant under normal planting but non-significant under late planting. Asymmetry of gene distribution among the parents was represented by significant b_2 component. Similarly, significant b_3 item indicated the important effect of specific genes. Influence of maternal and reciprocal effects (components c and d, respectively) was non-significant. Therefore re-testing of a and b items was not required.

The joint regression coefficient test indicated that under both normal and late plantings, regression coefficient differed significantly from zero but not from unity fulfilling the assumptions of the model. However, 2nd test which involves the analysis of variance of Wr + Vr and Wr-Vr for the confirmation of the absence of non-allelic interaction revealed significant differences for both Wr + Vr and Wr-Vr between arrays, indicating the presence of both dominance and non-allelic interaction. Therefore, the data were considered partially adequate to explain the genetic information in the presence of dominance and non-allelic interaction.

Genetic components of variation (Table-3) revealed significant values of both D and H components under both plantings suggesting that days to heading was under the control of both additive and dominance gene effects. Unequal values of H_1 and H_2 indicated the presence of positive and negative alleles in unequal frequencies. However, the difference was small in both cases. Component F was negative and non-significant under normal planting indicating lower frequency of dominant genes but non-significant under late planting. The environmental component of variation E was non-significant in both cases. Average degree of dominance was less than 1 indicating the absence of dominance for this trait under normal planting. The positive intercept of Wr/Vr regression line (Fig. 1a) also indicated an additive gene action with partial dominance. Average degree of dominance under late planting was more than 1 displaying an overdominant gene action. However, graphical representation of Wr/Vr regression (Fig. 1b) revealed a dominance gene action. Thus, the gene action changed from additive in normal

Table 1: Range of mean values for some growth parameters among wheat genotypes under normal and late planting showing mean reduction under late planting. Grand means in parenthesis.

	Days to heading (days)	Plant height (cm)	Fertile tillers per plant	Days to maturity (days)	Grain filling period (days)	Grain yield per plant (g)
Normal Planting	106.0-110.3 (108.5)	100.5-115.9 (109.7)	10.4-14.1 (12.3)	148.0-151.6 (150.0)	34.0-37.0 (35.7)	32.27-37.71 (34.93)
Late planting	87.0-92.3 (89.5)	80.1-93.3 (87.1)	7.8-11.6 (10.1)	125.3-128.0 (126.7)	28.3-31.6 (30.3)	21.71-26.98 (25.14)
Reduction (%)	17.50	20.60	17.67	15.54	15.25	28.04

Mahmood and Chowdhry: Heading, tillers, maturity, GFP, gene action, additive, dominance, wheat

Table 2: Analysis of variance of 6 × 6 diallel for the characters studied (Mean squares).

Items	df	Days to heading Normal	Days to heading Late	Plant height Normal	Plant height Late	Fertile tillers/plant Normal	Fertile tillers/plant Late	Days to maturity Normal	Days to maturity Late	Grain filling period Normal	Grain filling period Late	Grain yield/plant Normal	Grain yield/plant Late
a	5	34.9510**	33.6620**	242.100**	195.210**	21.440**	11.498**	8.352**	6.807**	11.529**	7.685**	19.006**	25.483**
b	15	2.3950**	3.6524**	78.853**	38.516**	1.404	1.476**	1.338**	1.949**	0.771*	3.849**	1.264	1.543
b_1	1	11.8510**	0.6685	86.616**	3.345	9.627*	0.535	2.535	1.557	3.337	1.157	9.753	0.631
b_2	5	1.5814*	3.0370**	72.702**	30.101*	1.171	0.456	2.009**	3.559**	0.615	2.431*	0.506	1.138
b_3	1	1.7962**	4.3259**	90.799**	37.846**	1.318	1.137**	-0.831	1.211*	0.770*	4.935**	1.454	2.021
c	5	0.3000	0.4444**	1.058	8.490	0.739	0.757	1.778	0.056	0.467	0.600	0.742	0.452
d	10	0.1333	0.0777	1.259	14.165	0.149	0.400	0.561	0.256	0.233	0.517	0.466	0.452
Blocks	2	0.2595	0.2870	10.986	23.858	1.180	0.467	3.787	0.260	0.343	1.565	5.835	1.587
B×a	10	0.1240	0.1407	13.331	8.663	0.808	0.363	1.191	0.763	0.791	0.246	1.542	1.440
B×b	30	0.2302	0.2561	7.606	6.925	0.918	0.292	0.373	0.406	0.314	0.380	0.651	1.232
B×b_1	2	0.0074	0.3129	2.214	0.470	0.617	0.232	0.624	0.807	0.369	0.502	0.698	0.441
B×b_2	10	0.3509	0.2092	5.206	6.626	0.877	0.270	0.212	0.437	0.395	0.412	0.529	0.930
B×b_3	18	0.1879	0.2759	9.538	7.808	0.975	0.311	0.434	0.344	0.262	0.349	0.713	1.488
B×c	10	0.1166	0.0777	7.808	8.543	1.152	0.699	1.294	0.422	0.783	0.583	0.676	0.805
B×d	20	0.275	0.2111	5.208	9.145	0.559	0.261	0.853	0.372	0.475	0.325	0.808	0.369
Block interactions	70	0.2116	0.2013	7.401	8.039	0.833	0.351	0.758	0.450	0.495	0.374	0.827	0.954

$* = P \leq 0.05$; $** = P < 0.01$

Table-3: Estimates of genetic components of variation under normal and late planting.

Components	Days to heading Normal	Days to heading Late	Plant height Normal	Plant height Late	Fertile tillers/plant Normal	Fertile tillers/plant Late	Days to maturity Normal	Days to maturity Late	Grain filling period Normal	Grain filling period Late	Grain yield/plant Normal	Grain yield/plant Late
D	2.08±0.14*	2.48±0.19*	18.49±3.78*	52.42±5.48*	1.16±0.15*	0.72±0.10*	0.96±0.17*	0.37±0.09*	1.29±0.08	0.74±0.21*	1.06±0.09*	2.99±0.11*
H_1	1.75±0.36*	2.92±0.48*	24.85±9.59*	62.09±13.90*	0.43±0.38	0.77±0.25*	0.58±0.43	1.69±0.21	0.21±0.20	2.745±0.54*	0.09±0.23	0.04±0.27
H_2	1.45±0.32*	2.29±0.42*	20.03±8.56*	47.59±12.42*	0.36±0.34	0.747±0.23	0.33±0.39	1.00±0.18	0.18±0.18	2.29±0.48*	0.19±0.21	0.18±0.24
F	-1.47±0.35*	-0.60±0.46	2.59±9.22	40.84±13.38*	-1.05±0.37*	-0.49±0.24*	0.38±0.42	0.35±0.20	0.09±0.19	0.38±0.52	-1.04±0.22	0.42±0.04
E	0.07±0.05	0.06±0.07	2.82±1.44	2.48±2.09*	0.28±0.05*	0.11±0.03*	0.28±0.06	0.14±0.03	0.16±0.03	0.13±0.08	0.16±0.26	0.32±0.04
$(H_1/D)^{0.5}$	0.91	1.08	1.15	1.03	0.60	1.03	0.782	2.13	0.40	1.92	0.30	0.12
h^2 (ns)	0.81	0.74	0.47	0.56	0.75	0.66	0.53	0.46	0.74	0.36	0.72	0.74
h^2 (bs)	0.97	0.97	0.90	0.84	0.81	0.87	0.64	0.80	0.80	0.87	0.76	0.76

$(H_1/D)^{0.5}$ = degree of dominance, h^2 (ns), (bs) = heritability in broad and narrow sense, respectively   * = Value is significant when it exceeds 1.96 after dividing it with its standard error.

planting to dominance under late planting. Additive gene action for this trait has earlier been reported by Raghuvanshi et al. (1988), Tandon et al. (1989) and Khan and Bajwa (1990) while Khurana et al. (1983) and Singh et al. (1987) reported both additive and dominant gene action for the trait.

High narrow and broad sense heritability estimates were also recorded (Table-3). Heritability in broad sense estimates the genetic proportion (additive + dominant + interaction) of the total phenotypic variation while heritability in narrow sense estimates only the additive proportion. Thus, broad-sense heritability estimates eventually are greater than narrow sense heritability. Their relative magnitude explicate the proportion of additive variation within genetic variation. Thus, for days to heading under normal planting, greater proportion of the heritable variation was of additive nature. Similarly, high estimates of heritability were also obtained under late planting. High estimates of broad and narrow sense heritability for days to heading were also reported by Ma (1988) and Raghuvanshi et al. (1988).

Placement of array points displayed (Fig. 1a) that LU26S had the maximum dominant genes for days to heading under normal planting. Genotypes 4072, Pak.81 and Fsd. 85 had the least dominant genes being farthest from the origin. Psbn.90 and 4943 occupied the intermediary position displaying equal proportion of dominant and recessive genes in them. Under late planting, Fig. 1c indicated that LU26S possessed the maximum number of dominant genes while maximum recessive genes were found in Fsd. 85 and Psbn.90.

To find out the correlated response of the dominant genes with the phenotype of the common parent, Wr + Vr values of the arrays were plotted against the parental values. Under normal planting (Fig. 1b), a positive correlation (0.892) clearly depicted that the parents with late heading had larger values of Wr + Vr and thus, had lesser dominant alleles. So early heading was under the control of dominant alleles. Similarly, Wr + Vr/P graph (Fig. 1d) under late planting depicted high positive correlation (0.767) between Wr + Vr and parental values (P). Thus, it was concluded that early heading was conditioned by dominant genes under both plantings.

Plant height: Analysis of variance for plant height under both plantings (Table-2) revealed highly significant and greater amount of additive (a) variation. Dominance variation (b) was also found significant. Component b_1 was non-significant under normal planting displaying the absence of directional dominance deviations of the genes while it was significant in case of late planting. Significant b_2 and b_3 items depicted asymmetry of gene distribution and important role of specific genes governing plant height. Asymmetry of gene distribution among parents for plant height was also reported by Singh and Singh (1992). Maternal (c) and reciprocal (d) effects were non-significant.

Retesting of a and b was thus, not needed.

Test of the regression coefficient b, showed that it differed significantly from zero but not from unity showing absence of non-allelic interaction and suggesting the adequacy of the data for the additive-dominance model for both plantings. But analysis of variance of array differences showed significant differences for Wr + Vr and Wr-Vr indicating presence of both dominance and non-allelic interaction under normal planting. However, these were non-significant under late planting. Thus, data were considered partially adequate for further analysis under normal planting and adequate under late planting. Iqbal et al. (1991) and Chowdhry et al. (1992) also provided the evidence of non-allelic interaction for plant height in wheat. When the genetic components of variation were computed (Table 3) it was revealed that both additive (D) and dominance effects (H) were significant under both plantings, however, magnitude of dominance was greater. Values of H_1 and H_2 were unequal in both planting indicating unequal distribution of positive and negative alleles among the parents. Significant and positive F value under normal planting signified the important role of dominant genes. Value of F under late planting was positive but non-significant. Environmental effect (E) was insignificant under both plantings. Average degree of dominance showed the presence of overdominance gene action under both plantings. Wr/Vr graph under normal planting (Fig. 2a) also indicated an overdominant gene action. However, under late planting Wr/Vr graph (Fig. 2) depicted presence of additive gene action with partial dominance. Results under normal planting are in accordance with those of Petrovic and Cermin (1994) who also reported overdominance gene action for this trait. While results under late planting are in accordance with those of Bebyakin and Korobova (1989), Chowdhry et al. (199), Lonc et al. (1993) and Lonc and Zalewski (1991) who reported additive gene action for plant height.

Broad sense heritability estimates were high (Table-2) while narrow sense heritability was about 52 percent of broad sense heritability under normal planting and percent under late planting. This indicated that about of the total inherited genetic portion was of dominant nature and half of additive nature.

According to the position of array points (Fig. 2a) Pak, 4072 and Psbn.90 had maximum dominant genes while 4943 and LU26S contained the maximum recessive genes under normal planting. In case of late planting (Fig. Pak. 81 and LU26S had maximum number of dominant genes while 4943 contained minimum number of dominant genes. Genotypes 4072, Fsd.85 and Psbn.90 occupied intermediary position.

Correlated response of parental phenotype with dominant genes (Fig. 2b) indicated that plant height under the control of dominant genes under normal planting which tended to increase the plant height. There Pak.81 and 4072 with greater dominant genes were
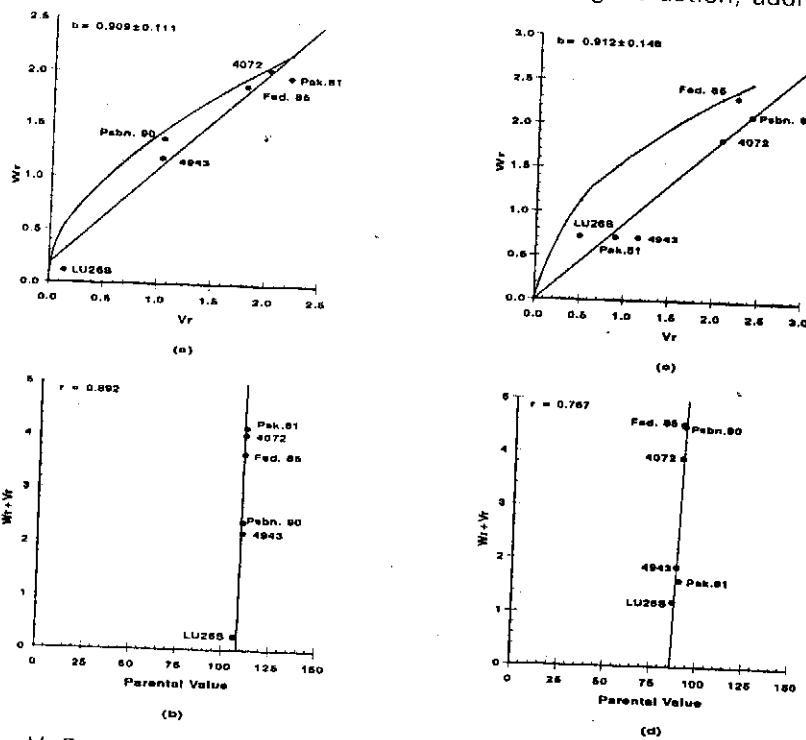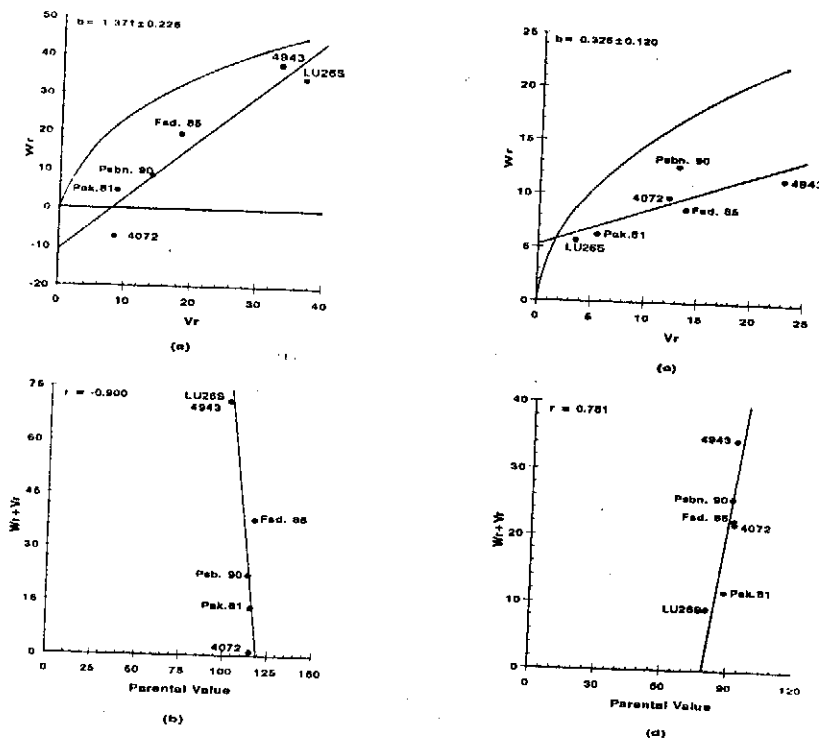
Fig. 1: Wr/Vr and Wr - Vr P graphs for days to heading under normal (a,b) and late planting (c,d)

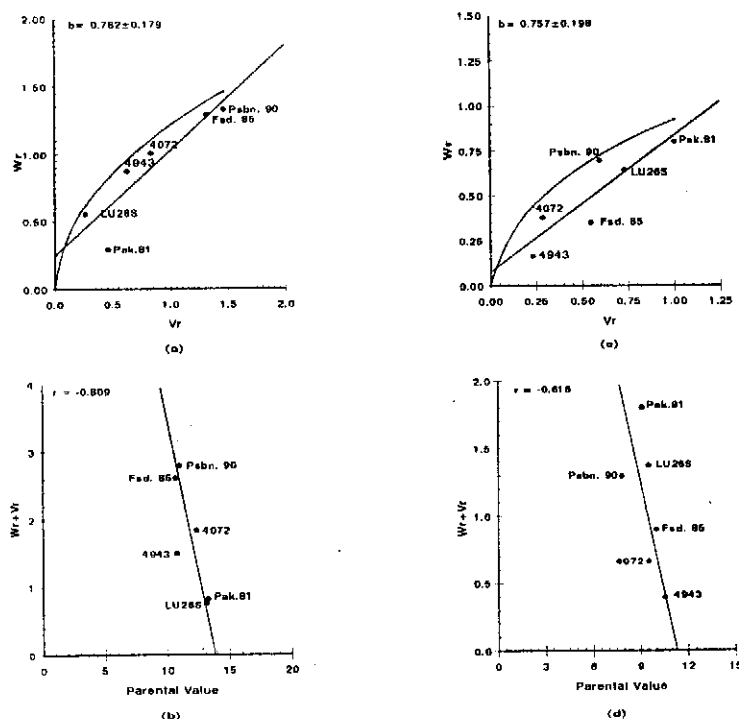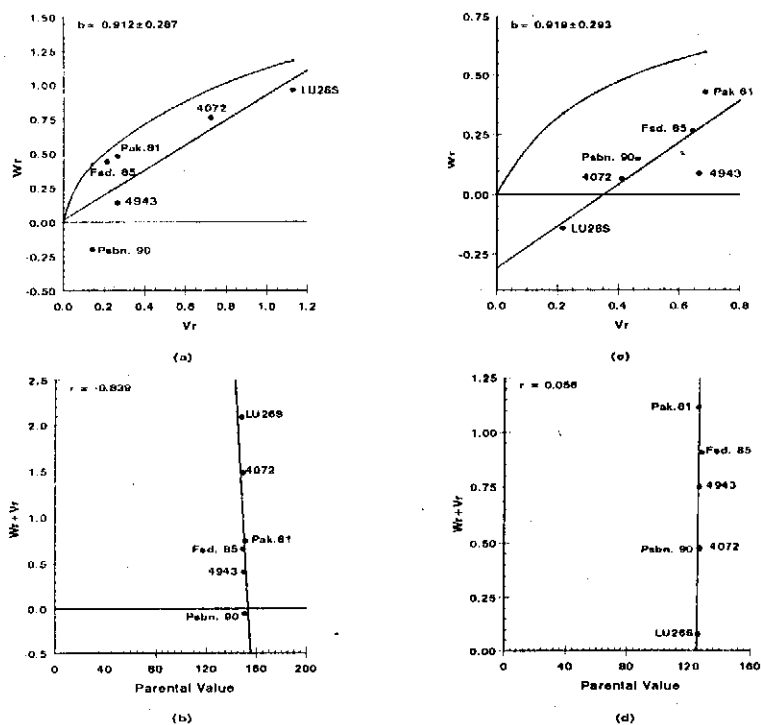2: Wr/Vr and Wr + Vr/P graphs for plant height under normal (a,b) and late planting (c,d)

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Fig. 3: Wr/Vr and Wr + Vr/P graphs for tillers per plant under normal (a,b) and late planting (c,d)

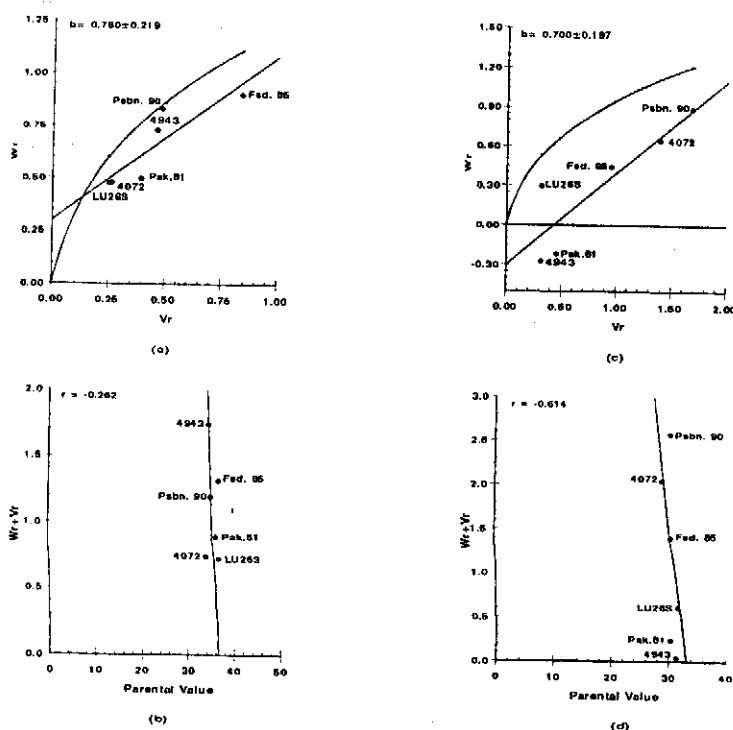Fig. 4: Wr/Vr and Wr + Vr/P graphs for days to maturity under normal (a,b) and late planting (c,d)

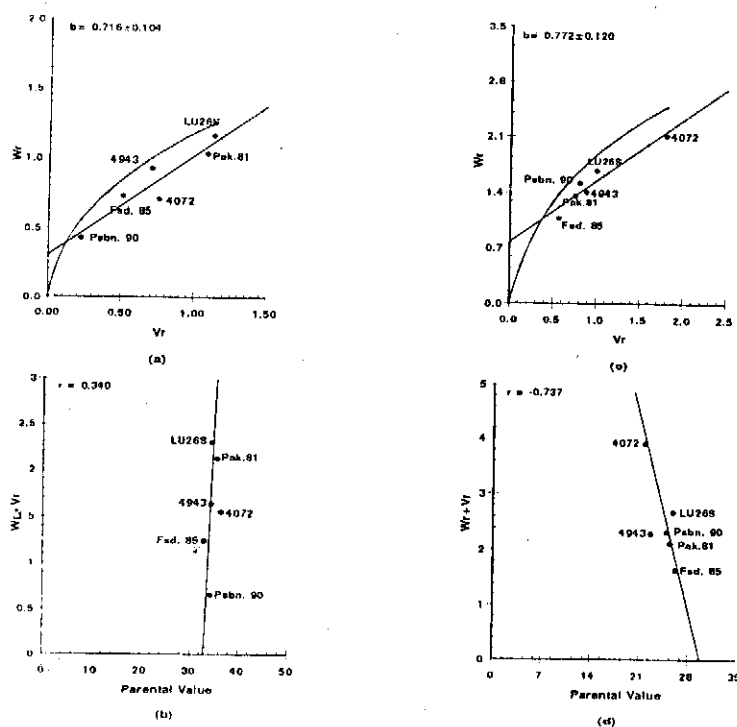Fig. 5: Wr/Vr and Wr + Vr/P graphs for grain filling period under normal (a,b) and late planting (c,d)

Fig. 6: Wr/Vr and Wr + Vr/P graphs for grain yield under normal (a,b) and late planting (c,d)

parents. Under late planting it became clear (Fig. 2d) that genes which lower the plant height were dominant while recessive genes were responsible for increasing the plant height. Thus, the parents with more recessive genes were taller.

Fertile tillers per plant: After carrying out formal diallel analysis (Table 2), it was observed that only the additive genetic effects (*a* component) were significant with equal frequency of dominant genes among the parents and absence of directional dominance under normal planting. Under late planting, both, additive (a) and dominant (b) gene effects were highly significant. Significant b_1 indicated the presence of directional dominance. Gene distribution among the parents was found symmetrical. Role of specific genes for this character under late planting was found significant. Retesting of *a* and *b* items was not required due to non-significant maternal and reciprocal effects.

Both scaling tests, regression coefficient and analysis of variance of Wr + Vr and Wr-Vr, indicated absence of dominance and non-allelic interaction. Thus, data were considered adequate for further computation for both plantings.

Genetic components of variation (Table 3) indicated that only additive component (**D**) was significant under normal planting. However, under late planting significant amount of both additive (**D**) as well as dominant (**H**) genetic variation was observed. The distribution of positive and negative alleles was different as indicated by H_1 and H_2 values under normal planting. While under late planting H_1 and H_2 values were necessarily equal showing similar distribution of positive and negative alleles in the parents. Negative and significant value of **F** under normal planting indicated the greater frequency of recessive genes as compared to dominant genes. Under late planting **F** was negative but non-significant. Environmental variation was significant in both plantings. Average degree of dominance under normal planting (0.609) indicated the absence of dominance. This was also shown by the graphical presentation of the data (Fig. 3a) where the intercept of regression lines was positive. Involvement of partial dominance with additive action for the trait has also been reported by Chowdhry *et al.* (1992) and Lonc *et al.* (1993).

Average degree of dominance under late planting (1.031), however, depicted over dominance gene action. In contrary, Wr/Vr graph (Fig. 3c) indicated an additive gene action with partial dominance. Dominance gene action for this trait was also reported by Prodanovic (1993) while Alam *et al.* (1990) and Lonc and Zalewski (1991) have reported overdominance gene action for tillers per plant.

Almost equal estimate of narrow and broad sense heritabilities under normal planting depicted that almost whole of the inherited genetic variation was of additive nature. The position of array points along the line (Fig. 3a) depicted that Pak. 81 had the maximum number of dominant genes while genotypes Psbn.90 and Fsd. 85 had

the lowest number of dominant genes under norm[al] planting. Genotypes 4072 and 4943 had nearly equ[al] number of dominant and recessive genes. Similarly, und[er] late planting (Fig. 3c), 4943 possessed most domina[nt] genes while Pak.81 possessed least dominant genes.

Correlated response (Fig. 3b & d), was negative (-0.80[ ] and -0.616) under both plantings. This suggested th[at] fertile tiller number was reduced due to recessive gen[es] while dominant genes were involved to increase them und[er] both plantings. Dominant gene control for tillers per pla[nt] was also reported by Lonc and Zlaewski (1991) whi[le] Jedynski (1988) reported a recessive gene control for th[is] trait.

Days to maturity: Analysis of variance for both planting[s] (Table-2) depicted aignificant additive (a) and dominant [b] effects, however, directional dominance (b_1) was absen[t]. Significant b_2 indicated different number of dominant gen[es] in the parents. Item b_3 was non-significant under norm[al] planting but significant in case of late planting displayi[ng] importance of specific gene effects in the later cas[e]. Maternal (c) and reciprocal (d) effects were non-significa[nt] in both plantings, thus, retesting of *a* and *b* items was n[ot] required.

When data were subjected to scaling tests adequacy of th[e] data was fulfilled by both tests under both plantings.

Components of genetic variation (Table 3) depict[ed] significant additive (**D**) variation while dominance was fou[nd] absent under normal planting. Under late planting, howeve[r] significant additive (**D**) as well as dominance (**H**) variati[on] was detected. Unequal values of H_1 & H_2 indicated unequ[al] distribution of positive and negative alleles in the paren[ts] under both plantings. Similarly, **F** was non-significant a[nd] positive. However, significant value of E depicted th[e] influence of environment on the expression of this tr[ait] under both plantings. Average degree of dominance (0.78[ ]) depicted the absence of complete dominance under norm[al] planting. The intercept of regression line in Wr/Vr gra[ph] (Fig. 4a) was also positive displaying the presence [of] partial dominance gene action. A greater portion of additi[ve] inherent variation was detectable from the narrow sen[se] heritability which was about 83.47 per cent of the bro[ad] sense heritability. Under late planting, however, averag[e] degree of dominance (2.139) indicated the involvement [of] an overdominant gene action. The Wr/Vr graph (Fig. [4c]) also displayed the same. The narrow sense heritabili[ty] estimate turn out to be 58.51 per cent of the broad sen[se] heritability suggesting the considerable involvement of bo[th] additive and dominant variation in the inheritance of days [to] maturity under late planting.

Fig. 4a further revealed that Psbn.90 and 4943 had [the] most dominant genes while LU26S had the low[est] dominant genes being farthest from the origin. Under l[ate] planting LU26S contained the most dominant genes for [the] character under study (Fig. 4c) while Pak.81 had [the] minimum number of dominant genes followed by Fsd.

Genotypes 4072 and Psbn.90 were located midway. The situation became more clear when correlated response of dominant gene distribution with the phenotype of the common parent was ascertained. A negative correlation (-0.839) indicated that dominant genes were responsible for increasing days to maturity while recessive genes decreased the time to mature under normal planting (Fig. 4b). The closeness of array points suggested the strength of this fact. Under late planting the correlated response of the dominant gene distribution with the phenotype of the common parent was positive (0.056). Thus, dominant genes seemed to lower the days to maturity while recessive genes increased them under late planting (Fig. 4d).

Grain filling period: Formal analysis of variance for grain filling period (Table 2) under both normal and late plantings indicated highly significant additive (a) and significant dominant (b) effects. Non-significant b_1 item indicated the absence of directional dominance. Item b_2 was non-significant under normal planting but significant under late planting. Significant b_3 component displayed the presence of specific gene effects under both plantings. Reciprocal (c) and maternal (d) effects were found absent.
Both scaling tests for the data under normal planting depicted absence of non-allelic interaction thus, data were fairly adequate for additive-dominance model. Under late planting regression coefficient b differed significantly from zero. However, analysis of variance of arrays indicated the presence of both dominance and non-allelic interaction between and within arrays. Thus, data were considered partially adequate.
Components of genetic variation (Table 3) indicated that under normal planting only additive variation (D) was significant while dominance was non-significant. However, under late planting these both components were significant; dominance being greater. H_1 and H_2 components were unequal showing different distribution of genes among parents in both plantings. F was non-significant and positive under both plantings. Environmental variance was significant under normal planting and non-significant under late planting. Average degree of dominance (0.408) under normal planting suggested the presence of partial dominance. Similarly, positive intercept of the regression line in Wr/Vr graph (Fig. 5a) also indicated partial dominance with additive gene action. High narrow sense heritability estimate (0.7446) also depicted the greater proportion of additive genetic variation as compared to dominance one in the total inherent genetic variation. However, average degree of dominance (1.927) under late planting presented an overdominant type of gene action. The regression line in Wr/Vr graph (Fig. 5c) also depicted the same gene action with negative intercept. Relatively small narrow sense heritability estimate in comparison with broad sense heritability also indicated greater amount of dominant inherited genetic variation.
The position of array points in Fig. 5a indicated that

LU26S, 4072 and Pak.81 had the most dominant genes while Fsd. 85 had the most recessive genes under normal planting. Psbn.90 and 4943 were located at intermediary position. Under late planting (Fig. 5c) maximum dominant genes were present in 4943, Pak.81 and LU26S while Psbn.90, being farthest from the origin, had the lowest dominant genes. Fsd. 85 was located in the middle having equal frequency of dominant and recessive genes.
Distribution of dominant genes was negatively correlated (-0.262 and -0.614) with the phenotype of the common parent (Fig. 5b and d) in case of both plantings which suggested that dominant genes were responsible to increase the grain filling period while recessive genes tended to decrease it. That is why the parents with most dominant genes had the smaller values of Wr + Vr. The arrangement of the parental values along the lines strongly confers this fact.

Grain yield per plant: Diallel analysis (Table 2) under both plantings revealed that only a item was significant indicating the presence of only additive gene effects with absence of directional dominance and symmetrical gene distribution and absence of any specific gene effects or maternal and reciprocal effects.
Both the scaling tests conducted (test of regression coefficient and analysis of arrays) revealed the absence of non-allelic interaction giving complete adequacy of the data for the additive-dominance model under both plantings.
Genetic components of variation (Table 3) revealed that only additive genetic variation was significant under both plantings. H_1 and H_2 values were different suggesting the asymmetry of positive and negative gene distribution. F was negative and significant under normal planting suggesting that the recessive genes were more frequent. Value of F under late planting was positive but non-significant. Average degree of dominance (0.302 and 0.125) indicated absence of dominance under both plantings. Graphical representation of the data (Fig. 6a & c) also depicted a similar gene action where the intercept of the regression line was positive.
Narrow-sense heritability under both planting was very high indicating the preponderance of additive genetic variation in the inheritance of this trait.
Location of array points in Fig. 6a indicated that Psbn.90 was the most dominant parent while LU26S and Pak.81 possessed the most recessive genes under normal planting. Under late planting Fsd. 85 was the parent with most dominant genes while genotype 4072 had the minimum dominant genes (Fig. 6c).
As displayed in Fig. 6b, recessive genes tended to increase the grain yield under normal planting. However, under late planting a dominant gene control for the trait was observed (Fig. 6d). Therefore, Fsd. 85 with maximum dominant genes had greater grain yield per plant. Similarly dominant gene control for grain yield per plant was also reported by Lonc and Zalewski (1991) while Lonc et al. (1993) reported

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recessive gene control for this trait.

These results revealed that genetic response of wheat genotypes for growth parameters was greatly influenced by the change in the planting time. Gene action for days to heading, days to maturity and grain filling period changed from additive under normal planting to dominant or overdominant under late planting. Similarly, heritability for these and other traits also varied under both planting conditions. Graphical representation depicted that parental genotypes changed their positions from dominant to recessive or midway, or from recessive to midway or dominant or the other way. This signifies the influential role of the environment on the genetic expression and inheritance of these growth parameters in wheat.

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